

# SEQUENCE LISTING

<110> Hitz, William  
 Sebastian, Scott  
 Grace, John  
 Streit, Leon

<120> SOYBEAN PLANT PRODUCING SEEDS WITH REDUCED LEVELS OF RAFFINOSE  
 SACCHARIDES AND PHYTIC ACID

<130> BB-1077-C

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 <151> APRIL 8, 1997

<150> PCT/US98/06822  
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35 40 45  
Val Lys Tyr Glu Phe Lys Thr Asn Ile His Val Pro Lys Leu Gly Val  
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Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Gly Gly  
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Val Ile Ala Asn Arg Glu Gly Ile Ser Trp Ala Thr Lys Asp Lys Ile  
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Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Ala Ile Arg  
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145 150 155 160  
Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu Ser Met Leu Pro  
165 170 175  
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180 185 190  
Arg Ala Asn Asn Val Ile Lys Gly Thr Lys Gln Glu Gln Val Gln Gln  
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Ile Ile Lys Asp Ile Lys Ala Phe Lys Glu Ala Thr Lys Val Asp Lys  
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Met Glu Asn Val Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val  
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Pro Gly Leu Ile Asp Leu Ala Ile Ala Arg Asn Thr Leu Ile Gly Gly  
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Asp Asp Phe Lys Ser Gly Gln Thr Lys Met Lys Ser Val Leu Val Asp  
305 310 315 320  
Phe Leu Val Gly Ala Gly Ile Lys Pro Thr Ser Ile Val Ser Tyr Asn  
325 330 335

His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe  
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 Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Asn  
 355 360 365  
 Ser Asn Ala Ile Leu Tyr Glu Pro Gly Glu His Pro Asp His Val Val  
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 Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp  
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 Glu Tyr Thr Ser Glu Ile Phe Met Gly Gly Lys Ser Thr Ile Val Leu  
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 His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp  
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 Asn Glu Gly Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu Ser  
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 Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn  
 465 470 475 480  
 Ala Leu Ser Lys Gln Arg Ala Met Leu Glu Asn Ile Met Arg Ala Cys  
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 <212> DNA  
 <213> Artificial Sequence

<220>  
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<210> 4  
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 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: synthetic oligonucleotide

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<210> 5  
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His Glu Asn Arg Asn Gly Thr Tyr Gln Trp Ile Val Lys Pro Lys Ser
  35             40             45

Val Lys Tyr Glu Phe Lys Thr Asn Ile His Val Pro Lys Leu Gly Val
  50             55             60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Gly Gly
  65             70             75             80

Val Ile Ala Asn Arg Glu Gly Ile Ser Trp Ala Thr Lys Asp Lys Ile
          85             90             95

Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Ala Ile Arg
 100             105             110

Val Gly Ser Phe Gln Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu
 115             120             125

Leu Pro Met Val Asn Pro Asp Asp Ile Val Phe Gly Gly Trp Asp Ile
 130             135             140

Ser Asn Met Asn Leu Ala Asp Ala Met Ala Arg Ala Lys Val Phe Asp
 145             150             155             160

Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu Ser Met Leu Pro
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Leu Pro Gly Ile Tyr Asp Pro Asp Phe Ile Ala Ala Asn Gln Glu Glu
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Arg Ala Asn Asn Val Ile Lys Gly Thr Lys Gln Glu Gln Val Gln Gln
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Val	Gly	Leu	Asn	Asp	Thr	Met	Glu	Asn	Leu	Leu	Ala	Ala	Val	Asp	Arg	245	250	255
Asn	Glu	Ala	Glu	Ile	Ser	Pro	Ser	Thr	Leu	Tyr	Ala	Ile	Ala	Cys	Val	260	265	270
Met	Glu	Asn	Val	Pro	Phe	Ile	Asn	Gly	Ser	Pro	Gln	Asn	Thr	Phe	Val	275	280	285
Pro	Gly	Leu	Ile	Asp	Leu	Ala	Ile	Ala	Arg	Asn	Thr	Leu	Ile	Gly	Gly	290	295	300
Asp	Asp	Phe	Lys	Ser	Gly	Gln	Thr	Lys	Met	Lys	Ser	Val	Leu	Val	Asp	305	310	315 320
Phe	Leu	Val	Gly	Ala	Gly	Ile	Lys	Pro	Thr	Ser	Ile	Val	Ser	Tyr	Asn	325	330	335
His	Leu	Gly	Asn	Asn	Asp	Gly	Met	Asn	Leu	Ser	Ala	Pro	Gln	Thr	Phe	340	345	350
Arg	Ser	Lys	Glu	Ile	Ser	Lys	Ser	Asn	Val	Val	Asp	Asp	Met	Val	Asn	355	360	365
Ser	Asn	Ala	Ile	Leu	Tyr	Glu	Pro	Gly	Glu	His	Pro	Asp	His	Val	Val	370	375	380
Val	Ile	Lys	Tyr	Val	Pro	Tyr	Val	Gly	Asp	Ser	Asn	Arg	Ala	Met	Asp	385	390	395 400
Glu	Tyr	Thr	Ser	Glu	Ile	Phe	Met	Gly	Gly	Lys	Ser	Thr	Ile	Val	Leu	405	410	415
His	Asn	Thr	Cys	Glu	Asp	Ser	Leu	Leu	Ala	Ala	Pro	Ile	Ile	Leu	Asp	420	425	430
Leu	Val	Leu	Leu	Ala	Glu	Leu	Ser	Thr	Arg	Ile	Glu	Phe	Lys	Ala	Glu	435	440	445
Asn	Glu	Gly	Lys	Phe	His	Ser	Phe	His	Pro	Val	Ala	Thr	Ile	Leu	Ser	450	455	460
Tyr	Leu	Thr	Lys	Ala	Pro	Leu	Val	Pro	Pro	Gly	Thr	Pro	Val	Val	Asn	465	470	475 480
Ala	Leu	Ser	Lys	Gln	Arg	Ala	Met	Leu	Glu	Asn	Ile	Met	Arg	Ala	Cys	485	490	495
Val	Gly	Leu	Ala	Pro	Glu	Asn	Asn	Met	Ile	Leu	Glu	Tyr	Lys			500	505	510

<210> 7

<211> 16

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<213> Artificial Sequence

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<223> Description of Artificial Sequence: synthetic oligonucleotide

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<210> 8  
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<220>  
<223> Description of Artificial Sequence: synthetic oligonucleotide

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His Glu Asn Arg Asn Gly Thr Tyr Gln Trp Ile Val Lys Pro Lys Ser  
35 40 45  
Val Lys Tyr Glu Phe Lys Thr Asn Ile His Val Pro Lys Leu Gly Val  
50 55 60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Gly Gly  
 65 70 75 80  
 Val Ile Ala Asn Arg Glu Gly Ile Ser Trp Ala Thr Lys Asp Lys Ile  
 85 90 95  
 Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Ala Ile Arg  
 100 105 110  
 Val Gly Ser Phe Gln Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu  
 115 120 125  
 Leu Pro Met Val Asn Pro Asp Asp Ile Val Phe Gly Gly Trp Asp Ile  
 130 135 140  
 Ser Asn Met Asn Leu Ala Asp Ala Met Ala Arg Ala Lys Val Phe Asp  
 145 150 155 160  
 Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu Ser Met Leu Pro  
 165 170 175  
 Leu Pro Gly Ile Tyr Asp Pro Asp Phe Ile Ala Ala Asn Gln Glu Glu  
 180 185 190  
 Arg Ala Asn Asn Val Ile Lys Gly Thr Lys Gln Glu Gln Val Gln Gln  
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 Ile Ile Lys Asp Ile Lys Ala Phe Lys Glu Ala Thr Lys Val Asp Lys  
 210 215 220  
 Val Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asn Leu Val  
 225 230 235 240  
 Val Gly Leu Asn Asp Thr Met Glu Asn Leu Leu Ala Ala Val Asp Arg  
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 Asn Glu Ala Glu Ile Ser Pro Ser Thr Leu Tyr Ala Ile Ala Cys Val  
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 Met Glu Asn Val Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val  
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 Pro Gly Leu Ile Asp Leu Ala Ile Ala Arg Asn Thr Leu Ile Gly Gly  
 290 295 300  
 Asp Asp Phe Lys Ser Gly Gln Thr Lys Met Lys Ser Val Leu Val Asp  
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 Phe Leu Val Gly Ala Gly Ile Lys Pro Thr Ser Ile Val Ser Tyr Asn  
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 His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe  
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 Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Asn  
 355 360 365  
 Ser Asn Ala Ile Leu Tyr Glu Pro Gly Glu His Pro Asp His Val Val  
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 Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp  
 385 390 395 400  
 Glu Tyr Thr Ser Glu Ile Phe Met Gly Gly Lys Ser Thr Ile Val Leu  
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His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp  
420 425 430

Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Glu Phe Lys Ala Glu  
435 440 445

Asn Glu Gly Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu Ser  
450 455 460

Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn  
465 470 475 480

Ala Leu Ser Lys Gln Arg Ala Met Leu Glu Asn Ile Met Arg Ala Cys  
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Val Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys  
500 505 510

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His Glu Asn Arg Asn Gly Thr Tyr Gln Trp Ile Val Lys Pro Lys Ser  
35 40 45



Val	Asn	Tyr	Gln	Phe	Lys	Thr	Asn	Thr	His	Val	Pro	Lys	Leu	Gly	Val	50	55	60
Met	Leu	Val	Gly	Trp	Gly	Gly	Asn	Asn	Gly	Ser	Thr	Leu	Thr	Gly	Gly	65	70	75
Val	Ile	Ala	Asn	Arg	Glu	Asp	Ile	Ser	Trp	Ala	Thr	Lys	Asp	Lys	Ile	85	90	95
Gln	Gln	Ala	Asn	Tyr	Phe	Gly	Ser	Leu	Thr	Gln	Ala	Ser	Ala	Ile	Arg	100	105	110
Val	Gly	Ser	Phe	Gln	Gly	Glu	Glu	Ile	Tyr	Ala	Pro	Phe	Lys	Ser	Leu	115	120	125
Leu	Pro	Met	Val	Asn	Pro	Asp	Asp	Ile	Val	Phe	Gly	Gly	Trp	Asp	Ile	130	135	140
Ser	Asn	Met	Asn	Leu	Ala	Asp	Ala	Met	Ala	Arg	Ala	Lys	Val	Phe	Asp	145	150	155
Ile	Asp	Leu	Gln	Lys	Gln	Leu	Arg	Pro	Tyr	Met	Glu	Ser	Met	Val	Pro	165	170	175
Leu	Pro	Gly	Ile	Tyr	Asp	Pro	Asp	Phe	Ile	Ala	Ala	Asn	Gln	Glu	Glu	180	185	190
Arg	Ala	Asn	Asn	Val	Ile	Lys	Gly	Thr	Lys	Gln	Glu	Gln	Val	Gln	Gln	195	200	205
Ile	Ile	Lys	Asp	Ile	Lys	Ala	Phe	Lys	Glu	Ala	Thr	Lys	Val	Asp	Lys	210	215	220
Val	Val	Val	Leu	Trp	Thr	Ala	Asn	Thr	Glu	Arg	Tyr	Ser	Asn	Leu	Val	225	230	235
Val	Gly	Leu	Asn	Asp	Thr	Met	Glu	Asn	Leu	Leu	Ala	Ala	Val	Asp	Arg	245	250	255
Asn	Glu	Ala	Glu	Ile	Ser	Pro	Ser	Thr	Leu	Tyr	Ala	Ile	Ala	Cys	Val	260	265	270
Met	Glu	Asn	Val	Pro	Phe	Ile	Asn	Gly	Ser	Pro	Gln	Asn	Thr	Phe	Val	275	280	285
Pro	Gly	Leu	Ile	Asp	Leu	Ala	Ile	Ala	Arg	Asn	Thr	Leu	Ile	Gly	Gly	290	295	300
Asp	Asp	Phe	Lys	Ser	Gly	Gln	Thr	Lys	Met	Lys	Ser	Val	Leu	Val	Asp	305	310	315
Phe	Leu	Val	Gly	Ala	Gly	Ile	Lys	Pro	Thr	Ser	Ile	Val	Ser	Tyr	Asn	325	330	335
His	Leu	Gly	Asn	Asn	Asp	Gly	Met	Asn	Leu	Ser	Ala	Pro	Gln	Thr	Phe	340	345	350
Arg	Ser	Lys	Glu	Ile	Ser	Lys	Ser	Asn	Val	Val	Asp	Asp	Met	Val	Asn	355	360	365
Ser	Asn	Ala	Ile	Leu	Tyr	Glu	Pro	Gly	Glu	His	Pro	Asp	His	Val	Val	370	375	380
Val	Ile	Lys	Tyr	Val	Pro	Tyr	Val	Gly	Asp	Ser	Lys	Arg	Ala	Met	Asp	385	390	395

Glu Tyr Thr Ser Glu Ile Phe Met Gly Gly Lys Asn Thr Ile Val Leu  
 405 410 415  
 His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp  
 420 425 430  
 Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Gln Phe Lys Ala Glu  
 435 440 445  
 Asn Glu Gly Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu Ser  
 450 455 460  
 Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn  
 465 470 475 480  
 Ala Leu Ser Lys Gln Arg Ala Met Leu Glu Asn Ile Met Arg Ala Cys  
 485 490 495  
 Val Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys  
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 <212> DNA  
 <213> Glycine max

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 cagtggattg tcaaacccaa atccgtcaac taccaattta aaaccaacac ccatgttcca 180  
 aaattggggg tgatgcttgt ggggttgggt ggaaacaacg gctctaccct caccggtggt 240  
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 tactttggct cctcaccaca agcctcagct attcgagttg gatccttcca gggagaggaa 360  
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 ggatgggata tcagcaacat gaacctggct gatgccatgg ccaggggcaaa ggtgtttgac 480  
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 aatgatggta tgaatctctc ggctccacaa accttccgct ccaaggaaat ctccaagagc 1080  
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 gacctatgtt ttgttattaa gtatgtgcct tacgtagggg atagcaagag agccatggat 1200  
 gagtacactt cagagatatt catgggtgga aagaacacca ttgttttgca caacacatgt 1260  
 gaggattccc ttttagctgc tctattatc ttggacttgg tccttcttgc tgagctgagc 1320  
 actagaatcc agtttaaagc tgaaaatgag ggaataattcc actcattcca cccagttgct 1380  
 accattctca gctatctgac caaggctcct ctggttccac cgggtacacc agtgggtgaat 1440  
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 ccagagaata acatgattct cgagtacaag tga 1533

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 <211> 510  
 <212> PRT  
 <213> Glycine max

<400> 14  
 Met Phe Ile Glu Asn Phe Lys Val Glu Ser Pro Asn Val Lys Tyr Thr  
 1 5 10 15  
 Glu Thr Glu Ile Gln Ser Val Tyr Asn Tyr Glu Thr Thr Glu Leu Val  
 20 25 30

11

Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp  
385 390 395 400

Glu Tyr Thr Ser Glu Ile Phe Met Gly Gly Lys Asn Thr Ile Val Leu  
405 410 415

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp  
420 425 430

Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Gln Phe Lys Ala Glu  
435 440 445

Asn Glu Gly Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu Ser  
450 455 460

Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn  
465 470 475 480

Ala Leu Ser Lys Gln Arg Ala Met Leu Glu Asn Ile Met Arg Ala Cys  
485 490 495

Val Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys  
500 505 510

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<211> 1533  
<212> DNA  
<213> Glycine max

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cagtggtattg tcaaacccaa atccgtcaac taccaattta aaaccaacac ccatgttcca 180  
aaattggggg tgatgcttgt ggggttggggg ggaacaacg gctctaccct caccgggtgt 240  
gttattgcta acagagaggg catttcattg gctacaaagg acaagattca acaagccaat 300  
tactttggct ccctcaccca agcctcagct attcgagttg gatccttcca gggagaggaa 360  
atctatgccc cattcaagag tctgcttcca atgggttaatc ctgacgacat tgtgtttggg 420  
ggatgggata tcagcaacat gaacctggct gatgccatgg ccagggcaaa ggtgtttgac 480  
atcgatttgc agaagcagtt gaggccttac atggaatcca tggttccact ccccggaatc 540  
tacgaccggg atttcattgc tgccaaccaa gaggagcgtg ccaacaacgt gattaagggc 600  
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aaagtggaca aggtggttgt cctgtggact gccaacacag agaggtatag caatttggtt 720  
gtaggcctta atgacaccat ggagaatctc ttggctgctg tggacagaaa tgaggctgag 780  
atttctcctt ccaccttcta tgccattgcc tgtgtgatgg aaaatgttcc ttccattaat 840  
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aacgttggtt acgatattgt caacagcaat gccatcctct atgagcctgg tgaacatccc 1140  
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gagtacactt cagagatatt catgggtgga aagaacacca ttgttttgca caacacatgt 1260  
gaggattccc ttttagctgc tcctattatc ttggacttgg tccttcttgc tgagctgagc 1320  
actagaatcc agtttaaagc tgaaaatgag ggaatttcc actcattcca cccagttgct 1380  
accattctca gctatctgac caaggctcct ctggttccac cgggtacacc agtgggtgaat 1440  
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ccagagaata acatgattct cgagtacaag tga 1533

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<212> PRT  
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 His Glu Asn Arg Asn Gly Thr Tyr Gln Trp Ile Val Lys Pro Lys Ser  
                     35                    40                    45  
 Val Asn Tyr Gln Phe Lys Thr Asn Thr His Val Pro Lys Leu Gly Val  
                     50                    55                    60  
 Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Gly Gly  
                     65                    70                    75                    80  
 Val Ile Ala Asn Arg Glu Gly Ile Ser Trp Ala Thr Lys Asp Lys Ile  
                     85                    90                    95  
 Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Ala Ile Arg  
                     100                    105                    110  
 Val Gly Ser Phe Gln Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu  
                     115                    120                    125  
 Leu Pro Met Val Asn Pro Asp Asp Ile Val Phe Gly Gly Trp Asp Ile  
                     130                    135                    140  
 Ser Asn Met Asn Leu Ala Asp Ala Met Ala Arg Ala Lys Val Phe Asp  
                     145                    150                    155                    160  
 Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu Ser Met Val Pro  
                     165                    170                    175  
 Leu Pro Gly Ile Tyr Asp Pro Asp Phe Ile Ala Ala Asn Gln Glu Glu  
                     180                    185                    190  
 Arg Ala Asn Asn Val Ile Lys Gly Thr Lys Gln Glu Gln Val Gln Gln  
                     195                    200                    205  
 Ile Ile Lys Asp Ile Lys Ala Phe Lys Glu Ala Thr Lys Val Asp Lys  
                     210                    215                    220  
 Val Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asn Leu Val  
                     225                    230                    235                    240  
 Val Gly Leu Asn Asp Thr Met Glu Asn Leu Leu Ala Ala Val Asp Arg  
                     245                    250                    255  
 Asn Glu Ala Glu Ile Ser Pro Ser Thr Leu Tyr Ala Ile Ala Cys Val  
                     260                    265                    270  
 Met Glu Asn Val Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val  
                     275                    280                    285  
 Pro Gly Leu Ile Asp Leu Ala Ile Ala Arg Asn Thr Leu Ile Gly Gly  
                     290                    295                    300  
 Asp Asp Phe Lys Ser Gly Gln Thr Lys Met Lys Ser Val Leu Val Asp  
                     305                    310                    315                    320  
 Phe Leu Val Gly Ala Gly Ile Lys Pro Thr Ser Ile Val Ser Tyr Asn  
                     325                    330                    335  
 His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe  
                     340                    345                    350  
 Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Asn  
                     355                    360                    365

Ser Asn Ala Ile Leu Tyr Glu Pro Gly Glu His Pro Asp His Val Val  
 370 375 380  
 Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp  
 385 390 395 400  
 Glu Tyr Thr Ser Glu Ile Phe Met Gly Gly Lys Asn Thr Ile Val Leu  
 405 410 415  
 His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp  
 420 425 430  
 Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Gln Phe Lys Ala Glu  
 435 440 445  
 Asn Glu Gly Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu Ser  
 450 455 460  
 Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn  
 465 470 475 480  
 Ala Leu Ser Lys Gln Arg Ala Met Leu Glu Asn Ile Met Arg Ala Cys  
 485 490 495  
 Val Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys  
 500 505 510